



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/761,983

DATE: 08/30/2004

TIME: 14:55:59

Input Set : N:\Cr3\RULE60\10761983.raw.txt

Output Set: N:\CRF4\08302004\J761983.raw

```

1 <110> APPLICANT: GONSALVES, DENNIS
2   LING, KAI-SHU
3 <120> TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
4   THEIR USES
5 <130> FILE REFERENCE: 07678/025007
6 <140> CURRENT APPLICATION NUMBER: US/10/761,983
7 <141> CURRENT FILING DATE: 2004-01-21
8 <150> PRIOR APPLICATION NUMBER: US/10/039,112
9 <151> PRIOR FILING DATE: 2002-12-31
10 <150> PRIOR APPLICATION NUMBER: US 09/650,324
11 <151> PRIOR FILING DATE: 2000-08-29
12 <150> PRIOR APPLICATION NUMBER: US 09/579,259
13 <151> PRIOR FILING DATE: 2000-05-25
14 <150> PRIOR APPLICATION NUMBER: US 09/224,898
15 <151> PRIOR FILING DATE: 1998-12-31
16 <150> PRIOR APPLICATION NUMBER: US 08/770,544
17 <151> PRIOR FILING DATE: 1996-12-20
18 <150> PRIOR APPLICATION NUMBER: US 60/009,008
19 <151> PRIOR FILING DATE: 1995-12-21
20 <160> NUMBER OF SEQ ID NOS: 67
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4173
25 <212> TYPE: DNA
26 <213> ORGANISM: Grapevine Leafroll Virus
27 <400> SEQUENCE: 1
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30   tcgggcattt ccgacaaact tgaacttcgg ggcgcgttcg acgtttctaa aaagaatttc 180
31   tccaggaggt tacgttcgag tcgtttgcgc gtattttcta gggctattgt ggaggatacg 240
32   atcaaggtta tgaaggcat gaaatcagag gatggtaaac cactccctat agccgaggat 300
33   tccgtgtacg cgttcatgac aggcaatatg tcaaacgttc attgcactag ggctggtttg 360
34   ctccggggct caaaggcttg cgcggcttct ttagctgtga aggggtgcagc ttcacgcgct 420
35   actggaacaa aactcttttc aggtctcaca tcttttctt ccgccgggtg tctgttttac 480
36   gatgaaggct tgacgcccg agagaggctt gatgcactaa cgcgccgtga acatgctgtg 540
37   aattcacctg taggcctctt agaacctgga gcttcggttg cgaagcgggt cgtttcgga 600
38   acgaaagctt ttctgtcaga attgtcattg gaggacttca ccactttcgt cataaaaaat 660
39   aggggtgctt ttggtgtttt tactctttcc atggctctca ctccgggtgt ctggaagtac 720
40   agaaggaata tcgcgcgaac tggcggtgat gttttccacc gtgctcggtc gggtaaccgcg 780
41   gccatcggtt tacaatgtct tagtgaggga aggtcggttag ctggtgacgc tgctcggtgc 840
42   gcgttaacag tgactcgagg agggctatct tcggcggttg cggtgaccag aaatacagtg 900
43   gctaggcgct aggtaccatt ggcgttgctt tcgttttcca cgtcttacgc agtcagtggc 960
44   tgcactttgt taggtatttg ggctcatgct ctccctagga atttgatgtt cttctttggc 1020

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ENTERED

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45 ctagggacgc tcttcgggggt gagtgccagt accaattctt ggtcgcttgg gggctatacg 1080
46 aacagtctgt tcaccgtacc ggaattaact tgggaagggg ggagttacag atctttattg 1140
47 cccaagcag ctttaggtat ttctctcggt gtgcgcgggt tgtaagtga aactgtgcca 1200
48 caactaacgt acgtaccgcc gattgaaggt cggaatgttt atgatacagg actaaatttt 1260
49 tatcgcgact ttgactatga cgatggtgca ggcccatccg ggacggctgg tcaaagcgat 1320
50 cctggaacca atacttcgga tactttctctg gttttctctg acgatggttt gcccgctagt 1380
51 ggcggtggct tcgacgcgcg cgttgaggca ggtcccagcc atgctgttga tgaatcacca 1440
52 aggggtagtg ttgagttcgt ctacagagaa cgtgtagatg aacatccggc gtgtggtgaa 1500
53 gctgaagttg aaaaggatct aataacacca cttggtacag ctgtcttaga gtcgcccccc 1560
54 gtaggtcctg aagctgggag cgcgcccac gtgcaggacg gttgtccgga ggttgaagct 1620
55 gagaaatgtt cggaggtcat cgttgacgtt cctagtccag aaccgccggg acaagaagtc 1680
56 cttgaatcaa ccaatggtgt ccaagctgca agaactgaag aggttgtgca gggcgacaca 1740
57 tgtggagctg gggtagctaa atcagaagtg agtcaacgtg tgtttcctgc gcaagtaccc 1800
58 gcacatgaag ctggtcttga ggcatactag ggcgcggtcg tggagccatt gcaagtttct 1860
59 gtgccagtag ccgtagagaa aactgtttta tctgtcgaga aggcgcgtga gctaaaggcg 1920
60 gtagataagg gcaaggcggg cgtgcacgca aaggaagtca agaattacc ggtaagacg 1980
61 ttaccacgag gggctctaaa aattagttag gataccgttc gtaaggaatt gtgcatgttt 2040
62 agaacgtgtt cctgcggcgt gcagttggag gtgtacaatg aagcgaccat cgccactagg 2100
63 ttctcaaatg cgtttacctt tgcgatagc ttgaaaggga ggagtgcggg ctttttctca 2160
64 aagctgggtg aggggtatag ctataatggt ggtagccatg tttcatcagg gtggcctcgt 2220
65 gccctagagg atattctaac ggcaattaag taccacagcg tcttcgacca ctgttttagt 2280
66 cagaagtaca agatgggtgg aggcgtacca ttccacgctg atgacgagga gtgctatcca 2340
67 tcagataacc ctatcttgac ggtcaatctc gtggggaagg caaacttctc gactaagtgc 2400
68 aggaaggggt gtaaggtcat ggtcataaac gtagcttcgg gtgactattt tcttatgcct 2460
69 tgcggttttc aaaggacgca cttgcattca gtaaaactca tcgacgaagg gcgcatcagt 2520
70 ttgacgttca gggcaactcg gcgcgtcttt ggtgtaggca ggatgttgca gttagccggc 2580
71 ggcgtgtcgg atgagaagtc accaggtgtt ccaaaccagc aaccacagag ccaaggtgct 2640
72 accagaacaa tcacacaaa atcggggggc aaggctctat ctgaggggag tggtagggaa 2700
73 gtcaagggga ggtcgacata ctcgatatgg tgcgaacaag attacgttag gaagtgtgag 2760
74 tggctcaggg ctgataatcc agtgatggct cttaaacctg gctacacccc aatgacattt 2820
75 gaagtggtta aagccgggac ctctgaagat gccgtcgtgg agtacttgaa gtatctggct 2880
76 ataggcattg ggaggacata cagggcgttg cttatggcta gaaatattgc cgtcactacc 2940
77 gccgaaggtg ttctgaaagt acctaatcaa gtttatgaat cactaccggg ctttcacgtt 3000
78 tacaagtcgg gcacagatct catttttcat tcaacacaag acggcttgcg tgtgagagac 3060
79 ctaccgtacg tattcatagc tgagaaaggt atttttatca agggcaaaga tgtcgacgcg 3120
80 gtagtagctt tgggcgacaa tctgtccgta tgtgatgata tattggtttt ccatgatgct 3180
81 attaatttga tgggtgcact gaaagtgtgt cgatgtggta tgggtgggtga atcatttaag 3240
82 tcgttcgaat acaaagtcta taatgctccc ccagggtggcg gtaagacgac gatgctagt 3300
83 gacgaatttg tcaagtcacc caatagcacg gccaccatta cggctaactg gggagttct 3360
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85 accacagtta actccagggt ggttaacttt attgtcaggg gaatgtataa aagggttttg 3480
86 gtggatgagg tgtacatgat gcatcaaggc ttactacaac taggcgtctt cgcaaccggc 3540
87 gcgtcggaag gcctcttttt tggagacata aatcagatac cattcataaa ccgggagaag 3600
88 gtgttttaga tggattgtgc tgtatttggt ccaaagaagg aaagcgttgt atacattct 3660
89 aaatcataca ggtgtccgtt agatgtttgc tacttgttgt cctcaatgac cgtaagggga 3720
90 acggaaaagt gttacctga aaaggtcgtt agcggtaagg acaaaccagt agtaagatcg 3780
91 ctgtccaaaa ggccaattgg aaccactgat gacgtagctg aaataaacgc tgacgtgtac 3840
92 ttgtgcatga ccagttgga gaagtcggat atgaagaggt cgttgaaggg aaaaggaaaa 3900
93 gaaacaccag tgatgacagt gcatgaagca cagggaaaaa cattcagtga tgtggtattg 3960

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94      tttaggacga agaaagccga tgactcccta ttcactaaac aaccgcatat acttgttggt 4020
95      ttgtcgagac acacacgctc actggtttat gccgctctga gctcagagtt ggacgataag 4080
96      gtcggcacat atattagcga cgcgtcgctt caatcagtat ccgacgcttt gcttcacacg 4140
97      ttcgccccgg ctggttgctt tcgaggtata tga                                4173
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 1390
101 <212> TYPE: PRT
102 <213> ORGANISM: Grapevine Leafroll Virus
103 <400> SEQUENCE: 2
104      Val Ser Thr Tyr Ala Lys Ser Val Met Asn Asp Asn Phe Asn Ile Leu
105      1          5          10          15
106      Glu Thr Leu Val Thr Leu Pro Lys Ser Phe Ile Val Lys Val Pro Gly
107      20          25          30
108      Ser Val Leu Val Ser Ile Thr Thr Ser Gly Ile Ser Asp Lys Leu Glu
109      35          40          45
110      Leu Arg Gly Ala Phe Asp Val Ser Lys Lys Asn Phe Ser Arg Arg Leu
111      50          55          60
112      Arg Ser Ser Arg Leu Arg Val Phe Ser Arg Ala Ile Val Glu Asp Thr
113      65          70          75          80
114      Ile Lys Val Met Lys Gly Met Lys Ser Glu Asp Gly Lys Pro Leu Pro
115      85          90          95
116      Ile Ala Glu Asp Ser Val Tyr Ala Phe Met Thr Gly Asn Met Ser Asn
117      100         105         110
118      Val His Cys Thr Arg Ala Gly Leu Leu Gly Gly Ser Lys Ala Cys Ala
119      115         120         125
120      Ala Ser Leu Ala Val Lys Gly Ala Ala Ser Arg Ala Thr Gly Thr Lys
121      130         135         140
122      Leu Phe Ser Gly Leu Thr Ser Phe Leu Ser Ala Gly Gly Leu Phe Tyr
123      145         150         155         160
124      Asp Glu Gly Leu Thr Pro Gly Glu Arg Leu Asp Ala Leu Thr Arg Arg
125      165         170         175
126      Glu His Ala Val Asn Ser Pro Val Gly Leu Leu Glu Pro Gly Ala Ser
127      180         185         190
128      Val Ala Lys Arg Val Val Ser Gly Thr Lys Ala Phe Leu Ser Glu Leu
129      195         200         205
130      Ser Leu Glu Asp Phe Thr Thr Phe Val Ile Lys Asn Arg Val Leu Ile
131      210         215         220
132      Gly Val Phe Thr Leu Ser Met Ala Leu Thr Pro Val Val Trp Lys Tyr
133      225         230         235         240
134      Arg Arg Asn Ile Ala Arg Thr Gly Val Asp Val Phe His Arg Ala Arg
135      245         250         255
136      Ser Gly Thr Ala Ala Ile Gly Leu Gln Cys Leu Ser Gly Gly Arg Ser
137      260         265         270
138      Leu Ala Gly Asp Ala Ala Arg Gly Ala Leu Thr Val Thr Arg Gly Gly
139      275         280         285
140      Leu Ser Ser Ala Val Ala Val Thr Arg Asn Thr Val Ala Arg Arg Gln
141      290         295         300
142      Val Pro Leu Ala Leu Leu Ser Phe Ser Thr Ser Tyr Ala Val Ser Gly
143      305         310         315         320

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```

144 Cys Thr Leu Leu Gly Ile Trp Ala His Ala Leu Pro Arg His Leu Met
145                               325                               330                               335
146 Phe Phe Phe Gly Leu Gly Thr Leu Phe Gly Val Ser Ala Ser Thr Asn
147                               340                               345                               350
148 Ser Trp Ser Leu Gly Gly Tyr Thr Asn Ser Leu Phe Thr Val Pro Glu
149                               355                               360                               365
150 Leu Thr Trp Glu Gly Arg Ser Tyr Arg Ser Leu Leu Pro Gln Ala Ala
151                               370                               375                               380
152 Leu Gly Ile Ser Leu Val Val Arg Gly Leu Leu Ser Glu Thr Val Pro
153                               385                               390                               395                               400
154 Gln Leu Thr Tyr Val Pro Pro Ile Glu Gly Arg Asn Val Tyr Asp Gln
155                               405                               410                               415
156 Ala Leu Asn Phe Tyr Arg Asp Phe Asp Tyr Asp Asp Gly Ala Gly Pro
157                               420                               425                               430
158 Ser Gly Thr Ala Gly Gln Ser Asp Pro Gly Thr Asn Thr Ser Asp Thr
159                               435                               440                               445
160 Ser Ser Val Phe Ser Asp Asp Gly Leu Pro Ala Ser Gly Gly Gly Phe
161                               450                               455                               460
162 Asp Ala Arg Val Glu Ala Gly Pro Ser His Ala Val Asp Glu Ser Pro
163                               465                               470                               475                               480
164 Arg Gly Ser Val Glu Phe Val Tyr Arg Glu Arg Val Asp Glu His Pro
165                               485                               490                               495
166 Ala Cys Gly Glu Ala Glu Val Glu Lys Asp Leu Ile Thr Pro Leu Gly
167                               500                               505                               510
168 Thr Ala Val Leu Glu Ser Pro Pro Val Gly Pro Glu Ala Gly Ser Ala
169                               515                               520                               525
170 Pro Asn Val Glu Asp Gly Cys Pro Glu Val Glu Ala Glu Lys Cys Ser
171                               530                               535                               540
172 Glu Val Ile Val Asp Val Pro Ser Ser Glu Pro Pro Val Gln Glu Val
173                               545                               550                               555                               560
174 Leu Glu Ser Thr Asn Gly Val Gln Ala Ala Arg Thr Glu Glu Val Val
175                               565                               570                               575
176 Gln Gly Asp Thr Cys Gly Ala Gly Val Ala Lys Ser Glu Val Ser Gln
177                               580                               585                               590
178 Arg Val Phe Pro Ala Gln Val Pro Ala His Glu Ala Gly Leu Glu Ala
179                               595                               600                               605
180 Ser Ser Gly Ala Val Val Glu Pro Leu Gln Val Ser Val Pro Val Ala
181                               610                               615                               620
182 Val Glu Lys Thr Val Leu Ser Val Glu Lys Ala Arg Glu Leu Lys Ala
183                               625                               630                               635                               640
184 Val Asp Lys Gly Lys Ala Val Val His Ala Lys Glu Val Lys Asn Val
185                               645                               650                               655
186 Pro Val Lys Thr Leu Pro Arg Gly Ala Leu Lys Ile Ser Glu Asp Thr
187                               660                               665                               670
188 Val Arg Lys Glu Leu Cys Met Phe Arg Thr Cys Ser Cys Gly Val Gln
189                               675                               680                               685
190 Leu Asp Val Tyr Asn Glu Ala Thr Ile Ala Thr Arg Phe Ser Asn Ala
191                               690                               695                               700
192 Phe Thr Phe Val Asp Ser Leu Lys Gly Arg Ser Ala Val Phe Phe Ser

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193	705	710	715	720
194	Lys Leu Gly Glu Gly Tyr Thr Tyr Asn Gly Gly Ser His Val Ser Ser			
195		725	730	735
196	Gly Trp Pro Arg Ala Leu Glu Asp Ile Leu Thr Ala Ile Lys Tyr Pro			
197		740	745	750
198	Ser Val Phe Asp His Cys Leu Val Gln Lys Tyr Lys Met Gly Gly Gly			
199		755	760	765
200	Val Pro Phe His Ala Asp Asp Glu Glu Cys Tyr Pro Ser Asp Asn Pro			
201		770	775	780
202	Ile Leu Thr Val Asn Leu Val Gly Lys Ala Asn Phe Ser Thr Lys Cys			
203		785	790	795
204	Arg Lys Gly Gly Lys Val Met Val Ile Asn Val Ala Ser Gly Asp Tyr			
205		805	810	815
206	Phe Leu Met Pro Cys Gly Phe Gln Arg Thr His Leu His Ser Val Asn			
207		820	825	830
208	Ser Ile Asp Glu Gly Arg Ile Ser Leu Thr Phe Arg Ala Thr Arg Arg			
209		835	840	845
210	Val Phe Gly Val Gly Arg Met Leu Gln Leu Ala Gly Gly Val Ser Asp			
211		850	855	860
212	Glu Lys Ser Pro Gly Val Pro Asn Gln Gln Pro Gln Ser Gln Gly Ala			
213		865	870	875
214	Thr Arg Thr Ile Thr Pro Lys Ser Gly Gly Lys Ala Leu Ser Glu Gly			
215		885	890	895
216	Ser Gly Arg Glu Val Lys Gly Arg Ser Thr Tyr Ser Ile Trp Cys Glu			
217		900	905	910
218	Gln Asp Tyr Val Arg Lys Cys Glu Trp Leu Arg Ala Asp Asn Pro Val			
219		915	920	925
220	Met Ala Leu Lys Pro Gly Tyr Thr Pro Met Thr Phe Glu Val Val Lys			
221		930	935	940
222	Ala Gly Thr Ser Glu Asp Ala Val Val Glu Tyr Leu Lys Tyr Leu Ala			
223		945	950	955
224	Ile Gly Ile Gly Arg Thr Tyr Arg Ala Leu Leu Met Ala Arg Asn Ile			
225		965	970	975
226	Ala Val Thr Thr Ala Glu Gly Val Leu Lys Val Pro Asn Gln Val Tyr			
227		980	985	990
228	Glu Ser Leu Pro Gly Phe His Val Tyr Lys Ser Gly Thr Asp Leu Ile			
229		995	1000	1005
230	Phe His Ser Thr Gln Asp Gly Leu Arg Val Arg Asp Leu Pro Tyr Val			
231		1010	1015	1020
232	Phe Ile Ala Glu Lys Gly Ile Phe Ile Lys Gly Lys Asp Val Asp Ala			
233		1025	1030	1035
234	Val Val Ala Leu Gly Asp Asn Leu Ser Val Cys Asp Asp Ile Leu Val			
235		1045	1050	1055
236	Phe His Asp Ala Ile Asn Leu Met Gly Ala Leu Lys Val Ala Arg Cys			
237		1060	1065	1070
238	Gly Met Val Gly Glu Ser Phe Lys Ser Phe Glu Tyr Lys Cys Tyr Asn			
239		1075	1080	1085
240	Ala Pro Pro Gly Gly Gly Lys Thr Thr Met Leu Val Asp Glu Phe Val			
241		1090	1095	1100

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 3,6,9,12,21,24

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10761983.raw.txt

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L:971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0